In the Specification:

Please amend the specification as shown:

Please delete the paragraphs on page 10, beginning at line 6 through page 11, line 3, and replace with the following paragraphs:

Figure 5 shows the DNA binding sites (A) and amino acid sequences (B) of multi-finger proteins previously selected by others, using methods other than the CSPO method of the present invention. These previously selected zinc finger proteins (B) were compared to CSPO-selected proteins designed to bind to the same DNA binding sites (A), as described in Examples 5, 6, and 7. Figure 5 A i) shows a binding site for BCR-ABL (SEQ ID NO.9). Aii) shows a binding site for erb-B2 (SEQ ID NO.11). A iii) shows a binding site in the HIV promoter (SEQ ID NO. 13). Figure 5 Bi) shows the recognition helix sequences of the Zf protein previously selected (by parallel selection) to bind to the BCR-ABL sequence shown in A i), as described in Example 5 **(SEQ ID NO: 8)**. B ii) shows the recognition helix sequences of the Zf protein previously selected (by parallel selelction) to bind to the erb-B2 sequence shown in A ii), as described in Example 6 **(SEQ ID NO: 10)**. B iii) shows the recognition helix sequences of the Zf protein previously selected (by bipartite selection) to bind to the HIV promoter sequence shown in A iii), as described in Example 7 **(SEQ ID NO: 12)**.

Figure 6 depicts recognition helix sequences of BCR-ABL target-binding Zfs selected using the CSPO methods of the present invention, and their activity in bacterial reporter gene expression assays, as described in Example 5. **Figure 6 discloses SEQ ID NOS: 8("wt") and 18-29, respectively, in order of appearance.**

Figure 7 depicts binding affinities and specificities (determined using EMSAs) for CSPO-selected BCR-ABL target-binding Zfs, as described in Example 5. **Figure 7 discloses SEQ ID NOS: 8, 18 and 24, respectively, in order of appearance.**

Figure 8 depicts recognition helix sequences of erb-B2 target-binding Zfs selected using the CSPO methods of the present invention, and their activity in bacterial reporter gene expression assays, as described in Example 6. **Figure 8 discloses SEQ ID NOS: 10 and 30-**

41, respectively, in order of appearance.

Figure 9 depicts binding affinities and specificities (determined using EMSAs) for the CSPO-selected erb-B2 target-binding Zfs described in Example 6. **Figure 9 discloses SEQ ID NOS: 10, 32 and 40, respectively, in order of appearance.**

Figure 10 depicts recognition helix sequences of HIV-1 promoter-binding Zfs selected using the CSPO methods of the present invention, and their activity in bacterial reporter gene expression assays, as described in Example 7. **Figure 10 discloses SEQ ID NOS: 12 and 42-53, respectively, in order of appearance.**

Figure 11 depicts binding affinities and specificities (determined using EMSAs) for the CSPO-selected HIV-1 promoter-binding Zfs described in Example 7. **Figure 11 discloses SEQ ID NOS: 12, 47 and 53, respectively, in order of appearance.**

Please delete the paragraph on page 66, lines 1-5 and replace it with the following paragraph:

Pairs of DNA oligonucleotides 25 base pairs in length were designed to contain 5' TTTT overhangs and a 10 bp BCR-ABL, erbB2, HIV, or Zif268 target binding site. Compatible oligonucleotides were annealed and radiolabeled with [α-^{32}P]dATP. The table below illustrates the primary strands of these oligonucleotide pairs:

	Binding site primary strand (5'-3')	SEQ ID NO
BCR-ABL	TTTTCGACAC**GCAGAAGCC**CATTAC	14
erbB2	TTTTCGACAA**GCCGCAGTG**GATTAC	15
HIV promoter	TTTTCGACAC**GATGCTGCA**TATTAC	16
Zif268	TTTTGACGGT**GCGTGGGCG**GTTCAC	17